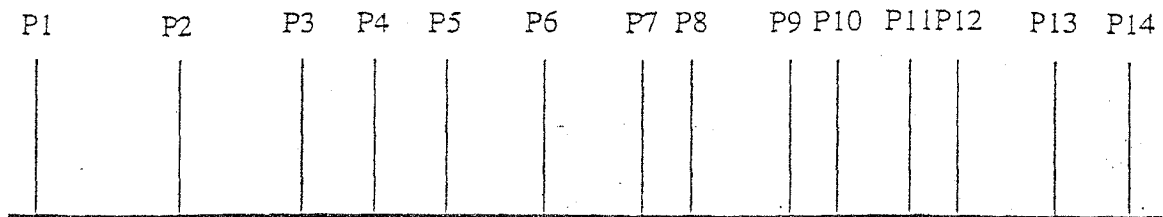
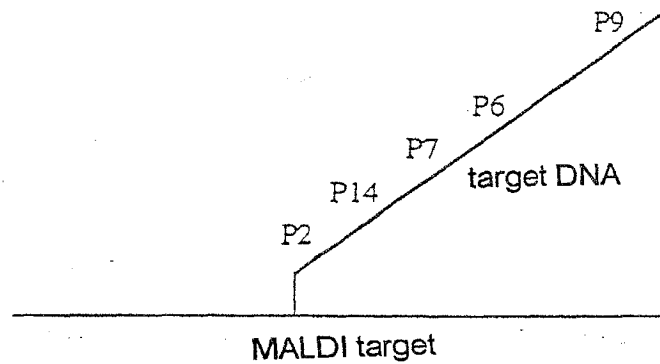


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1) Mass distribution of the probes



2) Hybridization



3) Mass distribution of hybridized probes

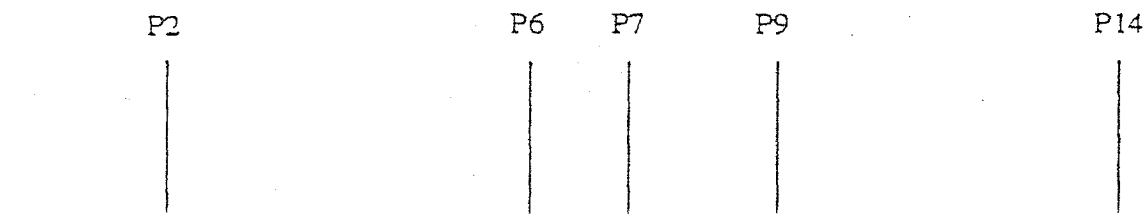


Fig. 1

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Immobilization of DNA directly on the MALDI target (example)

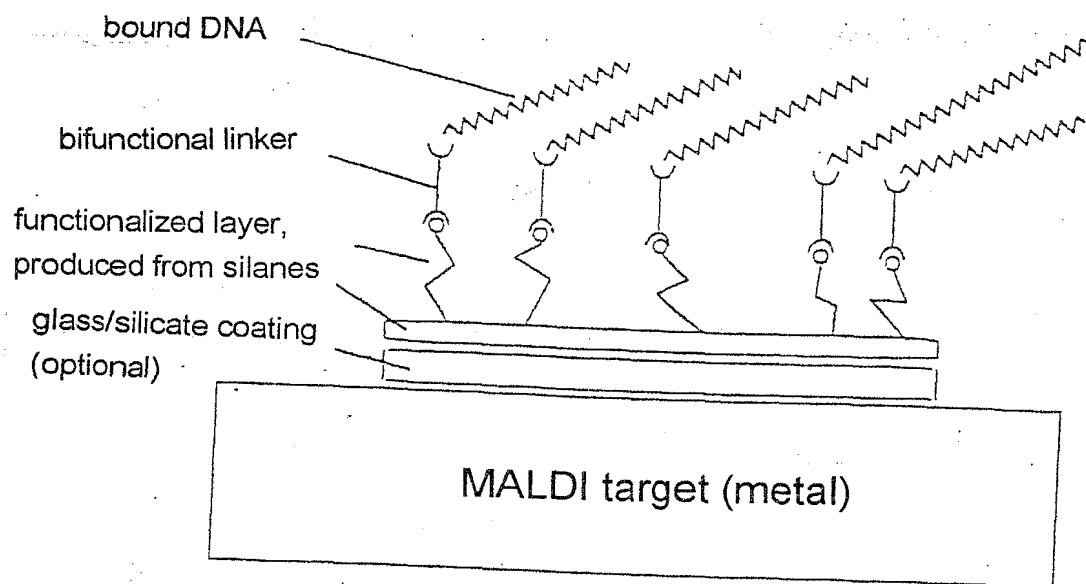
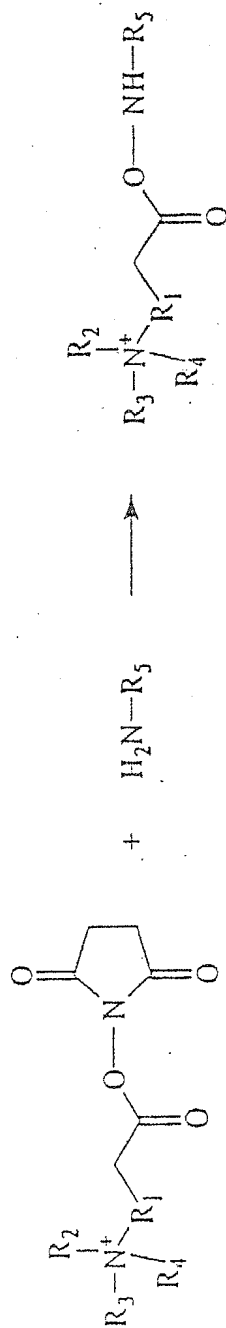


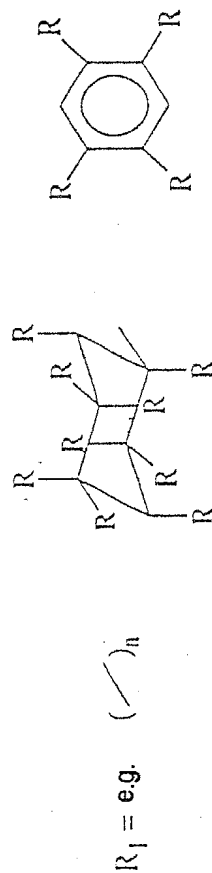
Fig. 2

N-terminal mass/charge tagging

Fig. 3



R = e.g. alkyl, -CH₃, -C₂H₅, -C₃H₇, -C₄H₉ etc.



R₂₋₄ = e.g. alkyl, substituted alkyl

R₅ = e.g. nucleic acid, PNA, methyl phosphonate nucleic acid, phosphorothioate nucleic acids

Fig. 4

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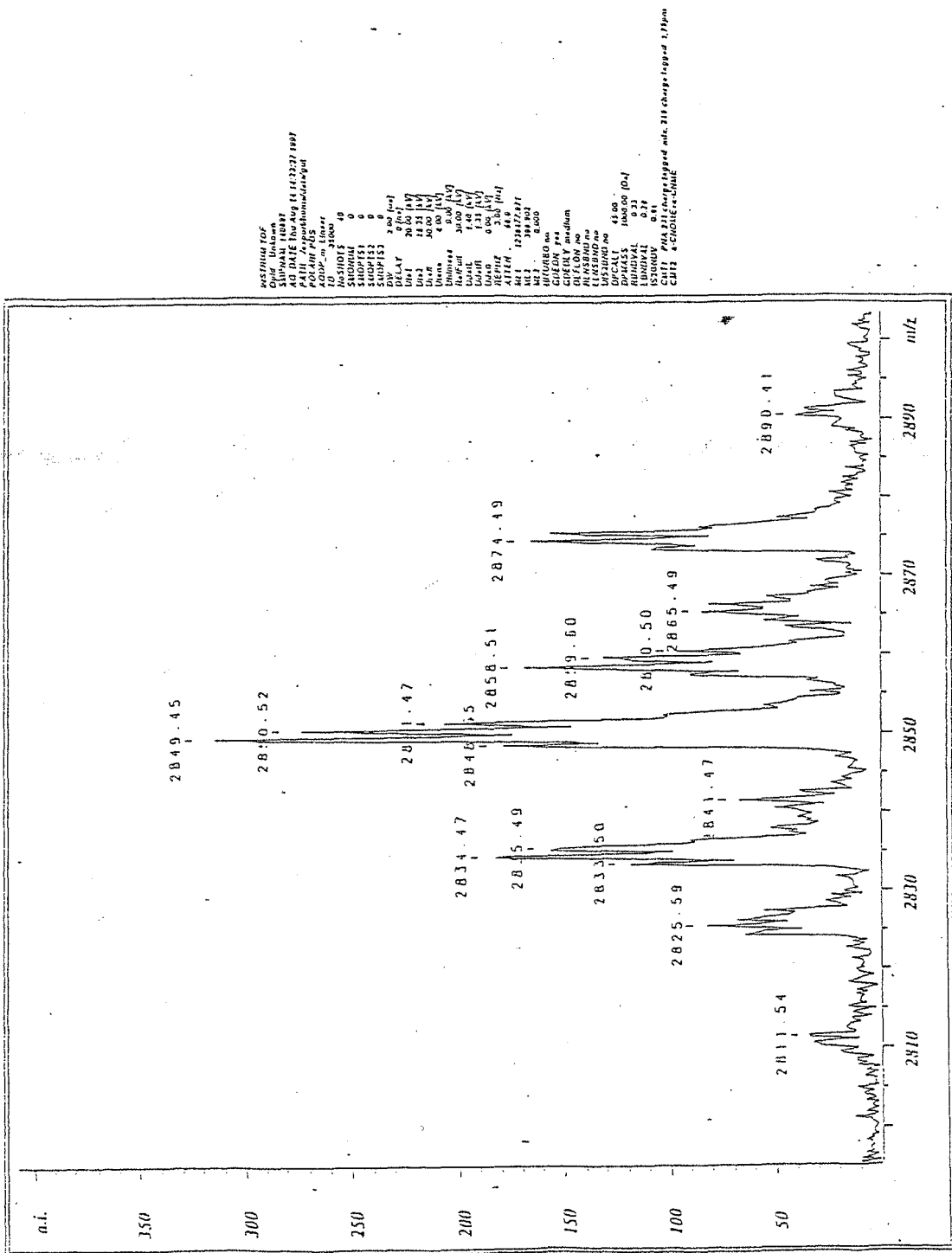
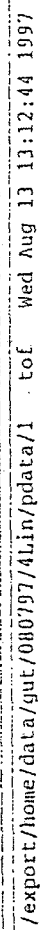


Fig. 5

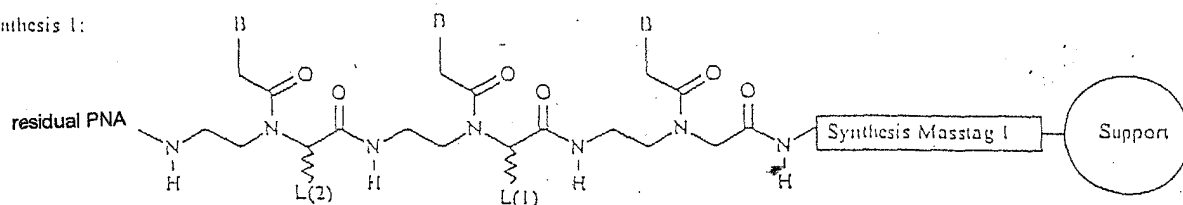
[illegible]

schon bald in den Händen der Polizei sein wird

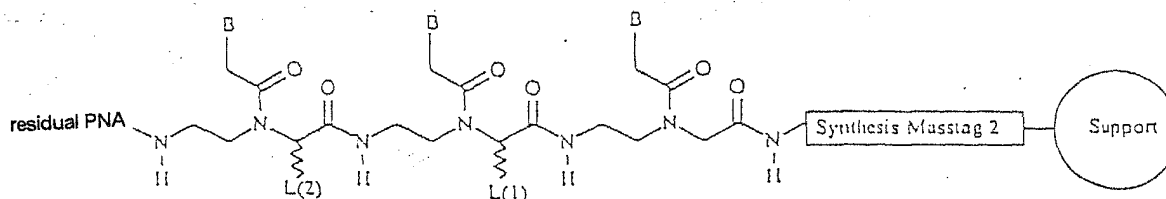
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Synthesis 1:



Synthesis 2:



....Synthesis n:



designed PNA library with
sequence-specific masses

B = adenine, cytosine, guanine, thymine or purine or pyrimidine derivatives or their deaza analogues

L(n) are various sets of substitutes, chosen specifically for each base which is used in each synthesis step in order to obtain minimized peak overlaps in the MALDI-MS

Fig. 7

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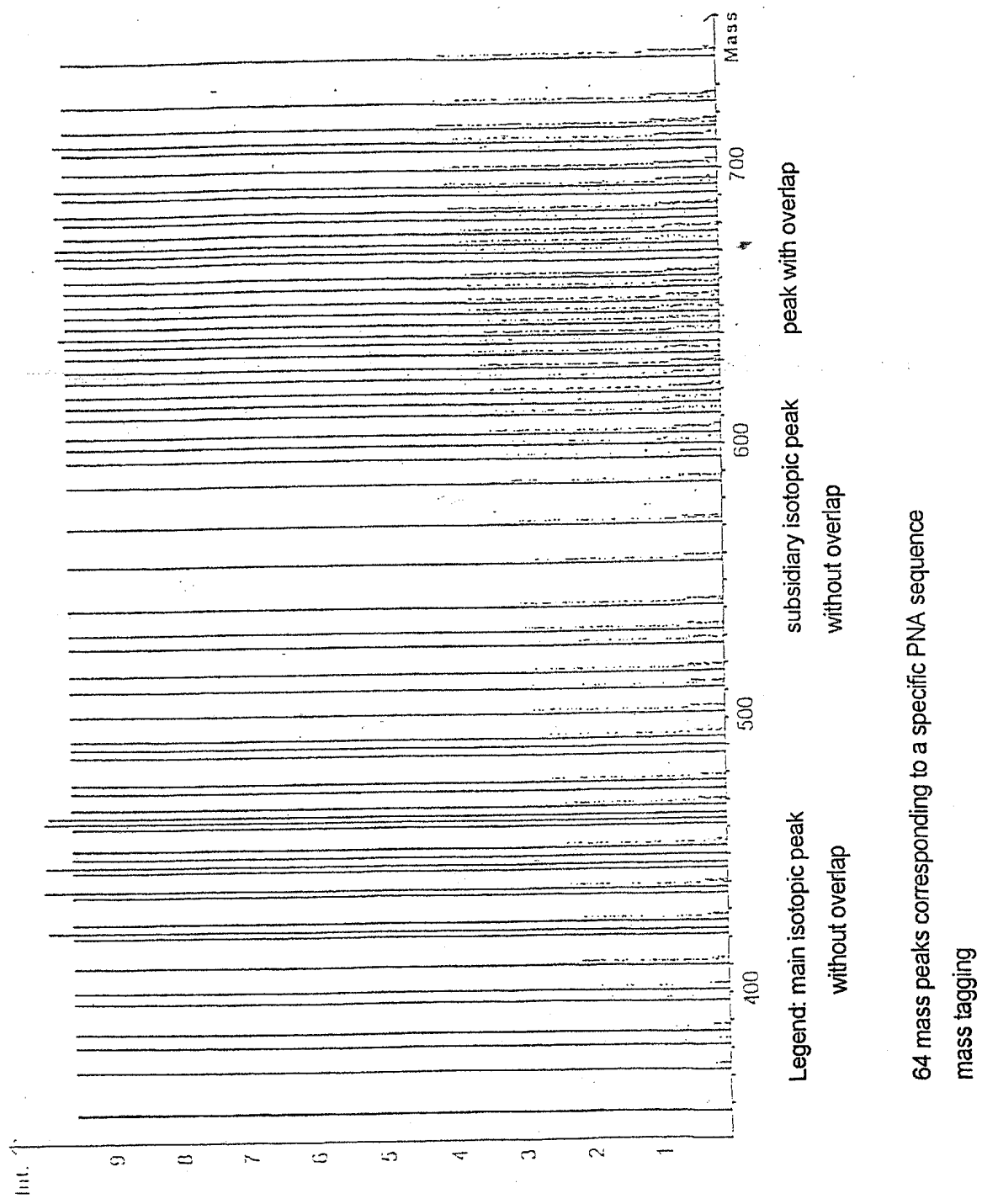


Fig. 8

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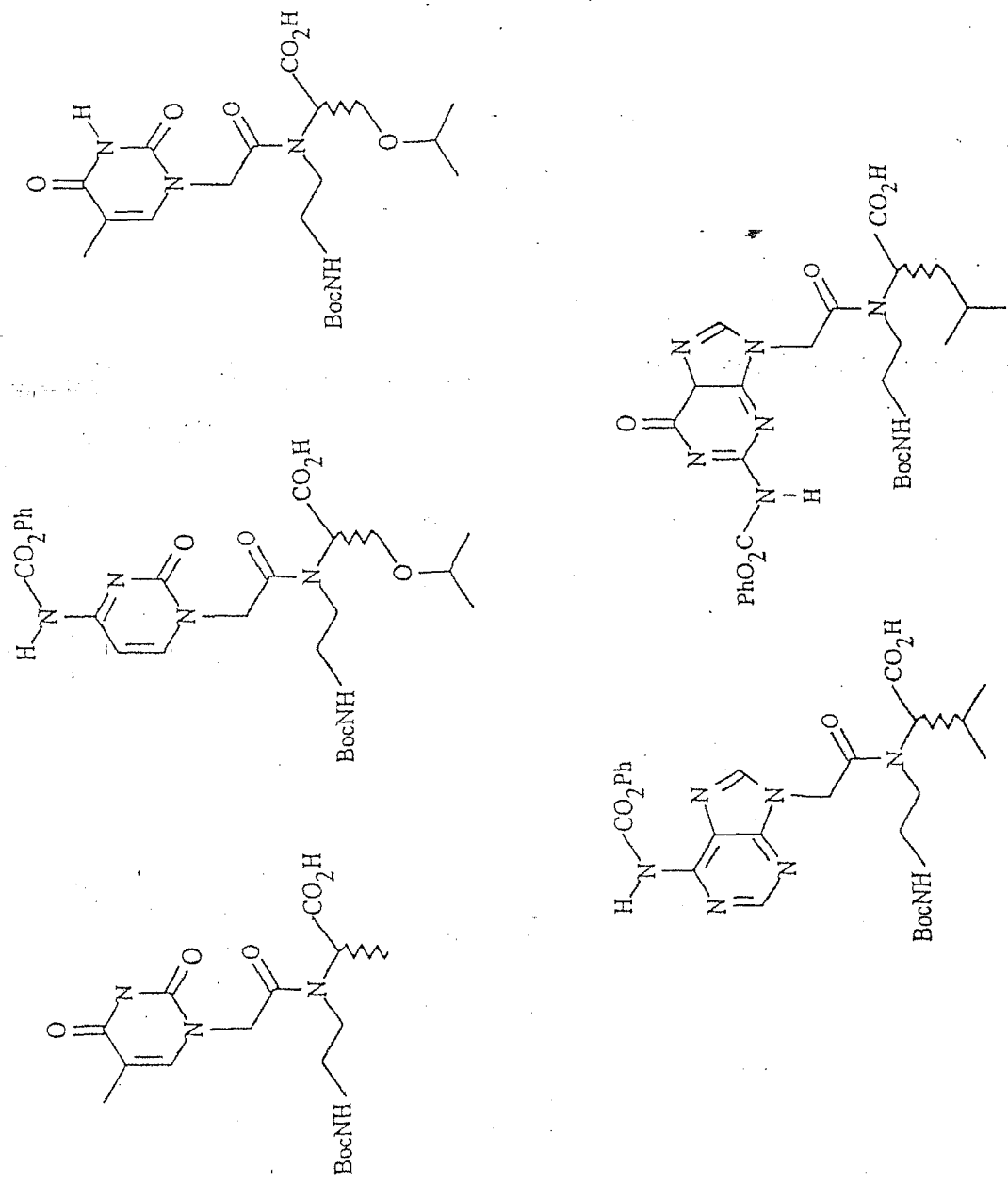


Fig. 9

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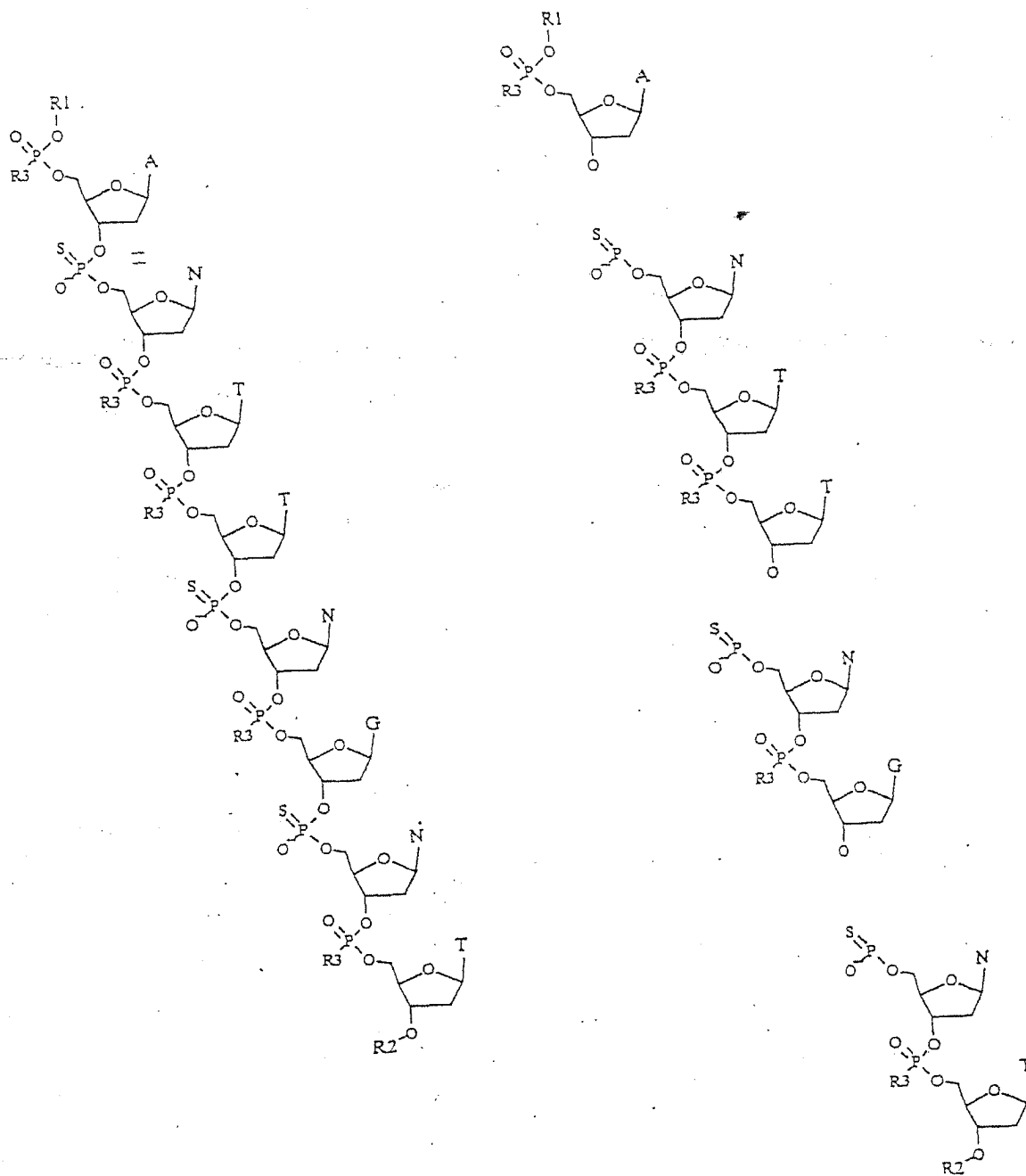
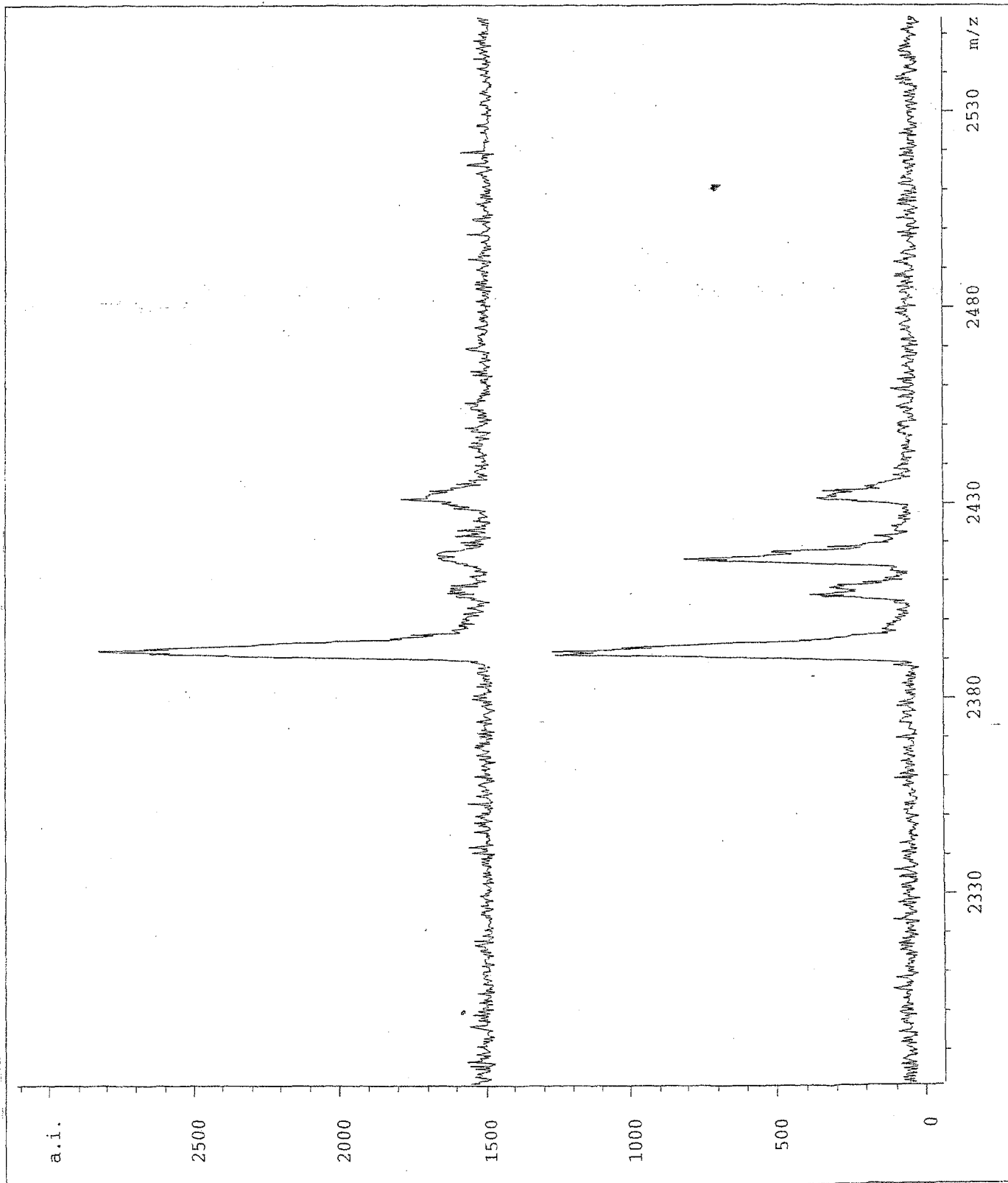


Fig. 10

Fig 11



INSTRUM TOF
Qp14 RCE
SMPNAM D41198
AQ_DATE Wed Dec 4 15:12:34 1998
EXPDIR /export/home/ramon/data/ramon
POLAR POS
ACQPT_m Linear
TD 35000
NBSLOTS 20
SNOCN 0
SNOPZ1 0
SNOPZ2 0
SNOPZ3 0
DW 2.00 [ns]
DELAY 0 [ns]
UIS1 20.00 [KV]
UIS2 18.20 [KV]
UIS3 11.00 [KV]
UIS4 7.00 [KV]
UIS5 0.00 [KV]
UIS6 0.00 [KV]
UIS7 21.00 [KV]
UIS8 1.50 [KV]
UIS9 1.45 [KV]
UIS10 2.00 [KV]
UIS11 1.00 [KV]
UIS12 80.00 [Hz]
NIS 1468145.233
NIS2 239.476
NIS3 0.000
HITURBO no
GREEN yes
GREENY short
DEFCON no
BLISSND no
BLISSND no
LANSND no
UIS2RND no
DPCALL 1.00
DPHASS 200.00 [Da]
RENOVAL 0.33
IS2RNDV 0.91
CHT1 start hyper. C, A and G with some T
CHT2 a-CH (C = compl.)

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09555866 11230000 09/555866

